



1/29

1
ATGGCTCCCTTAGCCGAAGTCGGGGGCTTTCTGGGCGGCCTGGAG
MetAlaProLeuAlaGluValGlyGlyPheLeuGlyGlyLeuGlu
46
GGCTTGGGCCAGCAGGTGGGTTCGCATTTCTGTGCTCCTGCC
GlyLeuGlyGlnGlnValGlySerHisPheLeuLeuProProAla
91
GGGGAGCGGCCGCGCTGCTGGGCGAGCGCAGGAGCGCGGCGGAG
GlyGluArgProProLeuLeuGlyGluArgArgSerAlaAlaGlu
136
CGGAGCGCGCGCGGGCCGGGGGCTGCGCAGCTGGCGCACCTG
ArgSerAlaArgGlyGlyProGlyAlaAlaGlnLeuAlaHisLeu
181
CACGGCATCCTGCGCCGCCGGCAGCTCTATTGCCGCACCGGCTTC
HisGlyIleLeuArgArgArgGlnLeuTyrCysArgThrGlyPhe
226
CACCTGCAGATCCTGCCCCACGGCAGCGTGCAGGGCACCCGGCAG
HisLeuGlnIleLeuProAspGlySerValGlnGlyThrArgGln
271
GACCACAGCCTCTTCGGTATCTTGAATTCATCAGTGTGGCAGTG
AspHisSerLeuPheGlyIleLeuGluPheIleSerValAlaVal
316
GGACTGGTCAGTATTAGAGGTGTGGACAGTGGTCTCTATCTTGA
GlyLeuValSerIleArgGlyValAspSerGlyLeuTyrLeuGly
361
ATGAATGACAAAGGAGAACTCTATGGATCAGAGAACTTACTTCC
MetAsnAspLysGlyGluLeuTyrGlySerGluLysLeuThrSer
406
GAATGCATCTTTAGGGAGCAGTTTGAAGAGAACTGGTATAACACC
GluCysIlePheArgGluGlnPheGluGluAsnTrpTyrAsnThr
451
TATTCATCTAACATATATAAACATGGAGACACTGGCCGCAGGTAT
TyrSerSerAsnIleTyrLysHisGlyAspThrGlyArgArgTyr
496
TTTGTGGCACTTAACAAAGACGGAACCTCCAAGAGATGGCGCCAGG
PheValAlaLeuAsnLysAspGlyThrProArgAspGlyAlaArg
541
TCCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTG
SerLysArgHisGlnLysPheThrHisPheLeuProArgProVal
586
GATCCAGAAAGAGTTCCAGAATTGTACAAGGACCTACTGATGTAC
AspProGluArgValProGluLeuTyrLysAspLeuLeuMetTyr
631
ACT
Thr

Fig. 1

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Query: 170 TGGCGCACCTGCACGGCATCCTGCGCCGCCGGCAGCTCTATTGCCGCACCGGCTTCCACC 229
| | | | | | | | | | | | | | | | | | | | | |
Sbjct: 2 TGGATCATTTAAAGGGGATTCTCAGGCGGAGGCAGCTATACTGCAGGACTGGATTTCACT 61

Query: 230 TGCAGATCCTGCCCCACGGCAGCGTGCAGGGCACCCGGCAGGACCACAGCCTCTTCGGTA 289
| | | | | | | | | | | | | | | | | | | | | |
Sbjct: 62 TAGAAATCTTCCCAATGGTACTATCCAGGGAACCAGGAAAGACCACAGCCGATTTGGCA 121

Query: 290 TCTTGGAATTCATCAGTGTGGCAGTGGGACTGGTCAGTATTAGAGGTGTGGACAGTGGTC 349
| | | | | | | | | | | | | | | | | | | | | |
Sbjct: 122 TTCTGGAATTTATCAGTATAGCAGTGGGCCTGGTCAGCATTCGAGGCGTGGACAGTGGAC 181

Query: 350 TCTATCTTGGAATGAATGACAAAGGAGAACTCTATGGATCAGAGAACTTACTTCCGAAT 409
| | | | | | | | | | | | | | | | | | | | | |
Sbjct: 182 TCTACCTCGGGATGAATGAGAAGGGGGAGCTGTATGGATCAGAAAACTAACCCAAGAGT 241

Query: 410 GCATCTTTAGGGAGCAGTTTGAAGAGAACTGGTATAACACCTATTCATCTAACATATATA 469
| | | | | | | | | | | | | | | | | | | | | |
Sbjct: 242 GTGTATTTCAGAGAACAGTTCGAAGAAAACCTGGTATAATACGTACTCGTCAAACCTATATA 301

Query: 470 AACATGGAGACACTGGCCGCAGGTATTTTGTGGCACTTAACAAAGACGGAACCTCCAAGAG 529
| | | | | | | | | | | | | | | | | | | | | |
Sbjct: 302 AGCACGTGGACACTGGAAGGCGATACTATGTTGCATTAAATAAAGATGGGACCCCGAGAG 361

Query: 530 ATGGCGCCAGGTCCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTGGATC 589
| | | | | | | | | | | | | | | | | | | | | |
Sbjct: 362 AAGGGACTAGGACTAAACGGCACCAGAAATTCACACATTTTTTACCTAGACCAGTGGACC 421

Query: 590 CAGA 593
| | |
Sbjct: 422 CCGA 425

Fig. 2

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>gb:GenBank accession number -ID:AB020858|acc:AB020858 Homo sapiens genomic DNA of p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 1/11 - Homo sapiens, 100000 bp.

Minus Strand HSPs:

A.

Score = 1430 (214.6 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126
Identities = 288/289 (99%), Positives = 288/289 (99%),
Strand = Minus / Plus

```
Query: 289 TACCGAAGAGGCTGTGGTCCTGCCGGGTGCCCTGCACGCTGCCGTCGGGCAGGATCTGCA 230
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 15927 TACCGAAGAGGCTGTGGTCCTGCCGGGTGCCCTGCACGCTGCCGTCGGGCAGGATCTGCA 15986

Query: 229 GGTGGAAGCCGGTGCGGCAATAGAGCTGCCGGCGGCGCAGGATGCCGTGCAGGTGCGCCA 170
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 15987 GGTGGAAGCCGGTGCGGCAATAGAGCTGCCGGCG-CGAGGATGCCGTGCAGGTGCGCCA 16045

Query: 169 GCTGCGCAGCCCCGGCCCCGCCGCGCGCTCCGCTCCGCCGCGCTCCTGCGCTCGCCCA 110
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 16046 GCTGCGCAGCCCCGGCCCCGCCGCGCGCTCCGCTCCGCCGCGCTCCTGCGCTCGCCCA 16105

Query: 109 GCAGCGGCGGCCGCTCCCCGGCAGGAGGCAACAGGAAATGCGAACCCACCTGCTGGCCCA 50
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 16106 GCAGCGGCGGCCGCTCCCCGGCAGGAGGCAACAGGAAATGCGAACCCACCTGCTGGCCCA 16165

Query: 49 AGCCCTCCAGGCCGCCAGAAAGCCCCCGACTTCGGCTAAGGGAGCCAT 1
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 16166 AGCCCTCCAGGCCGCCAGAAAGCCCCCGACTTCGGCTAAGGGAGCCAT 16214
```

B.

Score = 1224 (183.6 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126
Identities = 250/255 (98%), Positives = 250/255 (98%),
Strand = Minus / Plus

```
Query: 633 AGTGTACATCAGTAGGTCCTTGTACAATTCTGGAACCTTTTCTGGATCCACTGGTCTAGG 574
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 7257 AGTGTACATCAGTAGGTCCTTGTACAATTCTGGAACCTTTTCTGGATCCACTGGTCTAGG 7316

Query: 573 TAAGAAATGTGTAAATTTCTGATGCCTCTTGGACCTGGCGCCATCTCTTGGAGTTCCGTC 514
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 7317 TAAGAAATGTGTAAATTTCTGATGCCTCTTGGACCTGGCGCCATCTCTTGGAGTTCCGTC 7376

Query: 513 TTTGTTAAGTGCCACAAAATACCTGCGGCCAGTGTCTCCATGTTTATATATGTTAGATGA 454
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 7377 TTTGTTAAGTGCCACAAAATACCTGCGGCCAGTGTCTCCATGTTTATATATGTTAGATGA 7436

Query: 453 ATAGGTGTTATACCAGTTCTCTTCAAAGTCTCCCTAAAGATGCATTTCGGAAGTAAGTTT 394
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 7437 ATAGGTGTTATACCAGTTCTCTTCAAAGTCTCCCTAAAGATGCATTTCGGAAGTAAGTTT 7496
```

Fig.3

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QUERY: 393 CTC-TGATCCATAGA 380
 ||| ||| | |||
Sbjct: 7497 CTCCTGAAAGAGAGA 7511

C.
Score = 530 (75.9 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126
Identities = 106/106 (100%), Positives = 106/106 (100%),
Strand = Minus / Plus

QUERY: 391 CTGATCCATAGAGTTCTCCTTTGTCATTTCATTCCAAGATAGAGACCACTGTCCACACCTC 332
 |||||
Sbjct: 9837 CTGATCCATAGAGTTCTCCTTTGTCATTTCATTCCAAGATAGAGACCACTGTCCACACCTC 9896

QUERY: 331 TAATACTGACCAGTCCCCTGCCCACACTGATGAATTCCAAGATACC 286
 |||||
Sbjct: 9897 TAATACTGACCAGTCCCCTGCCCACACTGATGAATTCCAAGATACC 9942

Fig.3
(CONTINUED)

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Sequences analyzed:

1. HUMAN FGF-9 (P31371_HUMAN FGF-9) [SEQ ID NO:9]
2. MOUSE FGF-9 (P54130_MOUSE FGF-9) [SEQ ID NO:10]
3. RAT FGF-9 (P36364_FGF9_RAT FGF-9) [SEQ ID NO:11]
4. XENOPUS XFGF-CX (BAA83474Xen; Xenopus laevis XFGF-CX) [SEQ ID NO:12]
5. FGF-CX (cgAB020858) [SEQ ID NO:2]

Multiple Alignment:

HUMAN FGF-9	MAPLGEVGN ¹⁰ YFGVQDAVP--FGNVVPVP--VDSPVLLSDHLGQSEAGGLPRGPAVTDLDH
RAT FGF-9	MAPLGEVGS ¹⁰ YFGVQDAVP--FGNVVPVP--VDSPVLLSDHLGQSEAGGLPRGPAVTDLDH
MOUSE FGF-9	MAPLGEVGS ¹⁰ YFGVQDAVP--FGNVVPVP--VDSPVLLNDHLGQSEAGGLPRGPAVTDLDH
XENOPUS XFGF-CX	MAPLAD ¹⁰ VGCH ¹⁰ ELGGYDANG-QVGS ¹⁰ HF ¹⁰ LP ¹⁰ PAK ¹⁰ DS ¹⁰ PL ¹⁰ FN ¹⁰ DL ¹⁰ LA ¹⁰ SERLSR-SAP--SDLSH
FGF-CX	MAPLAEVGGELGGL ¹⁰ EG ¹⁰ LG ¹⁰ GG ¹⁰ QVGS ¹⁰ HF ¹⁰ LP ¹⁰ AG ¹⁰ ER ¹⁰ PL ¹⁰ LG ¹⁰ ERRSAAERSAR-GGPF ¹⁰ GA ¹⁰ Q ¹⁰ LAH
HUMAN FGF-9	LKGILRRRQLYCRTGPHLEIFPNGTIQTRKDHRSFGILEFISIAVGLVSIRGVDSGLYL
RAT FGF-9	LKGILRRRQLYCRTGPHLEIFPNGTIQTRKDHRSFGILEFISIAVGLVSIRGVDSGLYL
MOUSE FGF-9	LKGILRRRQLYCRTGPHLEIFPNGTIQTRKDHRSFGILEFISIAVGLVSIRGVDSGLYL
XENOPUS XFGF-CX	LQ ¹⁰ GILRRRQLYCRTGPHLQ ¹⁰ IL ¹⁰ PD ¹⁰ GN ¹⁰ Q ¹⁰ GTRQ ¹⁰ DHSRFGILEFISIA ¹⁰ W ¹⁰ AV ¹⁰ GLVSIRGVDTGLYL
FGF-CX	LHGILRRRQLYCRTGPHLQ ¹⁰ IL ¹⁰ PD ¹⁰ GS ¹⁰ VQ ¹⁰ GTRQ ¹⁰ DHSL ¹⁰ FGILEFISIAVGLVSIRGVDSGLYL
HUMAN FGF-9	GMNEKGELYGSEKLTQECVFREQFEENWYNTYSSNLYKHVDTGRRYYVALNKDGT ¹⁰ PREGT
RAT FGF-9	GMNEKGELYGSEKLTQECVFREQFEENWYNTYSSNLYKHVDTGRRYYVALNKDGT ¹⁰ PREGT
MOUSE FGF-9	GMNEKGELYGSEKLTQECVFREQFEENWYNTYSSNLYKHVDTGRRYYVALNKDGT ¹⁰ PREGT
XENOPUS XFGF-CX	GMND ¹⁰ KGEL ¹⁰ FG ¹⁰ SEKLT ¹⁰ SEC ¹⁰ VFREQFEENWYNTYSSNLYKHG ¹⁰ DS ¹⁰ GRRY ¹⁰ VALNKDGT ¹⁰ PRDGT
FGF-CX	GMND ¹⁰ KGELYGSEKLT ¹⁰ SEC ¹⁰ VFREQFEENWYNTYSSNLYKHG ¹⁰ DT ¹⁰ GRRY ¹⁰ VALNKDGT ¹⁰ PRDGA
HUMAN FGF-9	RTKR ¹⁰ HQKFT ¹⁰ HLPRPVD ¹⁰ DPDKVPELYKDIL ¹⁰ LSQS
RAT FGF-9	RTKR ¹⁰ HQKFT ¹⁰ HLPRPVD ¹⁰ DPDKVPELYKDIL ¹⁰ LSQS
MOUSE FGF-9	RTKR ¹⁰ HQKFT ¹⁰ HLPRPVD ¹⁰ DPDKVPELYKDIL ¹⁰ LSQS
XENOPUS XFGF-CX	RA ¹⁰ KR ¹⁰ HQKFT ¹⁰ HLPRPVD ¹⁰ PE ¹⁰ KVPELYKD ¹⁰ IM ¹⁰ GY ¹⁰ S
FGF-CX	RS ¹⁰ KR ¹⁰ HQKFT ¹⁰ HLPRPVD ¹⁰ PER ¹⁰ VPELYKD ¹⁰ EL ¹⁰ LMY ¹⁰ LS

Fig. 4



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Fig. 5



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ptnr:SWISSPROT-ACC:P31371 GLIA-ACTIVATING FACTOR PRECURSOR (GAF) (FIBROBLAST GROWTH FACTOR-9)
(FGF-9) (HBGF-9) - HOMO SAPIENS (HUMAN), 208 aa. Identities = 147/208 (70%), Positives = 170/208
(81%)

```
Query:      1 MAPLAEVGGFLGGLEGLGQQVGSFLLPPAGERPPLLGERRSAAERSARG-GPGAAQLAH 59
             ||||| ||| + | + + | + + | | + | || + + | ||
Sbjct:      1 MAPLGEVGNFYFGVQDAV--PFGNVPVLPV--DSPVLLSDHLGQSEAGGLPRGPAVTDLDH 56

Query:     60 LHGILPRRQLYCRTGFHLQILPDGSVQGTRQDHSLFGILEFISVAVGLVSIRGVDSGLYL 119
             | ||||| ||||| ||||| ||| + | + + | + | || ||||| ||| + | ||||| ||||| |||
Sbjct:     57 LKGILRRRQLYCRTGFHLEIFPNGTIQGTRKDHSRFGILEFISIAVGLVSIRGVDSGLYL 116

Query:    120 GMNDKGELYGSEKLTSECFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA 179
             ||| + ||||| ||||| ||| + ||||| ||||| ||||| + ||| ||||| + ||||| ||||| + |
Sbjct:    117 GMNEKGELYGSEKLTQECVFREQFEENWYNTYSSNLYKHVDTGRRYYVALNKDGTPREGT 176

Query:    180 RSKRHQKFTHFLPRPVDPERVPELYKDIL 208
             | + ||||| ||||| ||||| ++ ||||| ||| + |
Sbjct:    177 RTKRHQKFTHFLPRPVDPKVPELYKDIL 205
```

Fig. 6

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LENGTH = 208

Plus Strand HSPs:

Score = 775 (272.8 bits), Expect = 3.4e-76, P = 3.4e-76
Identities = 147/208 (70%), Positives = 170/208 (81%), Frame = +1

Query: 1 MAPLAEVGGFLGGLEGLGQQVGSFLLPPAGERPPLLGERRSAAERSARG-GPGAAQLAH 59
||||| ||| + | + + | + + || + | || + + | ||
Sbjct: 1 MAPLGEVGSYFGVQDAV--PFGNVPVLPV--DSPVLLNDHLGQSEAGGLPRGPAVTDLDH 56

Query: 60 LHGILRRRQLYCRTGFHLQILPDGSVQGTRQDHSFGILEFISVAVGLVSIRGVDSGLYL 119
| ||||| ||||| ||||| + | + | ++ ||| + ||| ||||| ||||| + ||||| ||||| |||||
Sbjct: 57 LKGILRRRQLYCRTGFHLEIFPNGTIQGTRKDHSRFGILEFISIAVGLVSIRGVDSGLYL 116

Query: 120 GMNDKGELYGSEKLTSECFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA 179
||| + ||||| ||||| ||| + ||||| ||||| ||||| + ||| ||||| ||||| + |||
Sbjct: 117 GMNEKGELYGSEKLTQECVFREQFEENWYNTYSSNLYKHVDTGRRYYVALNKDGTREGT 176

Query: 180 RSKRHQKFTHFLPRPVDPERVPELYKDIL 208
| + ||||| ||||| ||||| ++ ||||| ||| + |
Sbjct: 177 RTKRHQKFTHFLPRPVDPKVPELYKDIL 205

Fig. 7



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Length = 208

Plus Strand HSPs:

Score = 775 (272.8 bits), Expect = 3.4e-76, P = 3.4e-76
Identities = 147/208 (70%), Positives = 170/208 (81%), Frame = +1

```
Query:   1 MAPLAEVGGFLGGLEGLGQQVGSFLLPPAGERPPLLGERSSAAERSARG-GPGAAQLAH 59
          ||||| ||| + | + + | + + || + || + + | ||
Sbjct:   1 MAPLGEVGSYFGVQDAV--PFGNVPVLPV--DSPVLLSDHLGQSEAGGLPRGPAVTDLDH 56

Query:  60 LHGILRRRQLYCRTGFHLQILPDGSVQGTQDHSLEFGILEFISVAVGLVSIRGVDSGLYL 119
          | ||||| ||||| ||||| + | + | ++ ||| + ||| ||||| ||||| + ||||| |||||
Sbjct:  57 LKGILRRRQLYCRTGFHLEIFPNGTIQGTQDHSRFGILEFISIAVGLVSIRGVDSGLYL 116

Query:  120 GMNDKGELYGSEKLTSECIFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA 179
          ||| + ||||| ||||| ||| + ||||| ||||| ||||| + ||||| ||||| + |||||
Sbjct:  117 GMNEKGELYGSEKLTQECVFREQFEENWYNTYSSNLYKHVDTGRRYYVALNKDGTREGT 176

Query:  180 RSKRHQKFTHFLPRPVDPERVPELYKDIL 208
          | + ||||| ||||| ||||| ++ ||||| + |
Sbjct:  177 RTKRHQKFTHFLPRPVDPKVPELYKDIL 205
```

Fig. 8

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FGF-CX Query Length = 211
XFGF-CX Sbjct Length = 208

Plus Strand HSPs:

Score = 906 (318.9 bits), Expect = 4.4e-90, P= 4.4e-90
Identities = 170/211 (80%), Positives = 189/211 (89%), Frame = +1

```
Query:   1 MAPLAEVGGFLGGLEGLGQQVGSFLLPPAGERPPLLGERRSAAERSARGGPGAAQLAHL 60
          |||||+|| |||| + ||| ||||| ||||| + | | + + + || + | | + |||
Sbjct:   1 MAPLADVGTFLGGYDALGQ-VGSFLLPPAKDSPLL FNDPLAQSERLSRSAP--SDLSHL 57

Query:  61 HGILRRRQLYCRTGFHLQILPDGQVQTRQDHSFGILEFISVAVGLVSIRGVDSGLYL 120
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:  58 QGILRRRQLYCRTGFHLQILPDGNVQTRQDHSRFGILEFISVAIGLVSIRGVDTGLYL 117

Query: 121 MNDKGELYGSEKLTSECFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRD 180
          ||||| + ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 118 MNDKGELFGSEKLTSECFREQFEENWYNTYSSNLYKHGDSGRRYFVALNKDGTPRD 177

Query: 181 SKRHQKFTHFLPRPVDPERVPELYKDLLMYT 211
          + ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 178 AKRHQKFTHFLPRPVDPEKVPPELYKDLMGYS 208
```

Fig. 9

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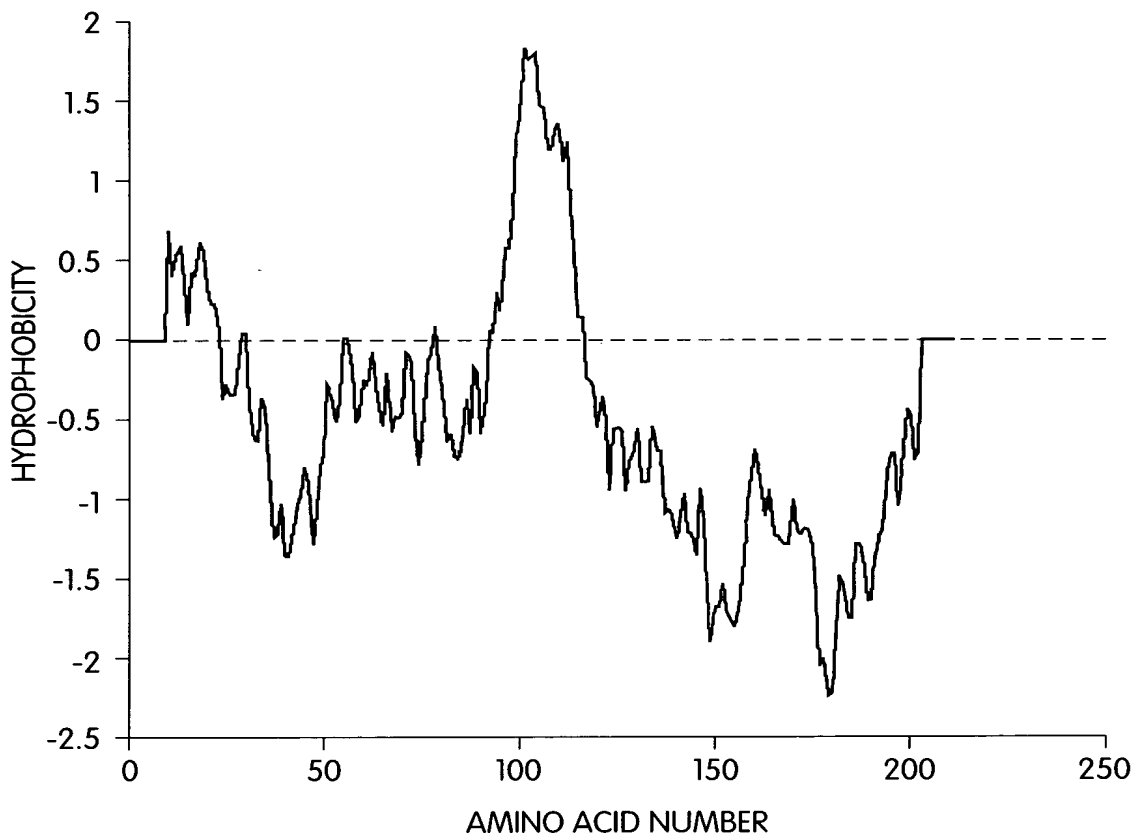


Fig. 10

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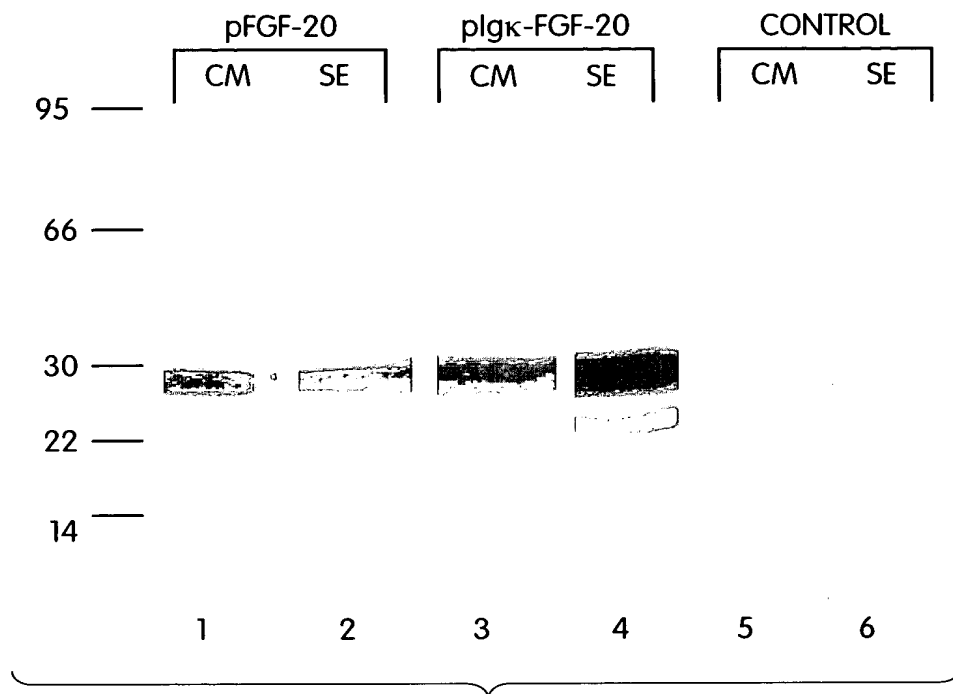


Fig. 11A

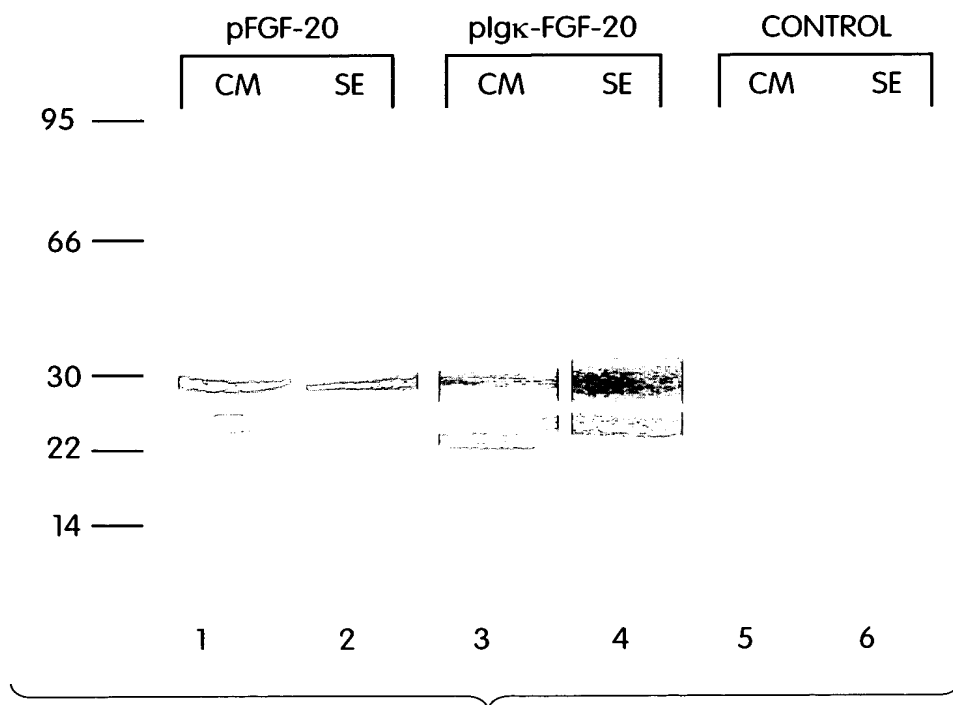


Fig. 11B

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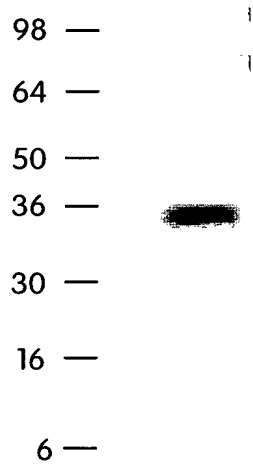
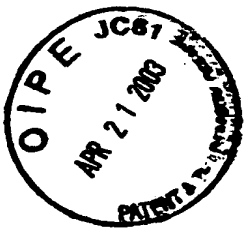


Fig. 12

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Exon 1

...AGACAGTGAGACTTCCTGCCATTTCAGTGCAAGTCCCTCCGGAGCGACCTCAGAGAGTAACCGGGCGCTTAAC

TTTTGGCGCTCGTTTGGCTATAAATTTTCTCTATCCACTCCCATCCACCCCAACACTCTTTACTGGGGGGGCTTTT

GTGTTCCGGATCTCCCCCTCCATGGCTCCCTTAGCGGAAGTCGGGGGGCTTCTGGGGGGCTGGAGGCTTGGGCCAGCA

1 M A P L A E V G G F L G G L E G L G Q Q

GGTGGGTTCCGATTTCTGTGCTCCTGCGGGGAGCGGCCCGCTGCTGGCGAGCGCAGGAGCGCGGGGAGCGGA

21 V G S H F L L P P A G E R P P L L G E R R S A A E R S

GCGCGCGCGGGGGGGGCTGCGCAGCTGGCGCACCTGCACGGCATCTCGCGCGCGCGCAGCTTATTCGCGCAC

48 A R G G P G A A Q L A H L H G I L R R R Q L Y C R T

GGCTTCCACTGCAGATCTGCCGACGCGGTGCAGGGCACCGCGGAGCACACAGCTCTTCGGTATCTTGGAAAT

<-|-> Exon 2

74 G F H L Q I L P D G S V Q G T R Q D H S L F G I L E F

CATCAGTGTGGCAGTGGACTGGTCAGTATTAGAGTGTGGACAGTGGTCTCTATCTTGGATGAATGACAAAGGAGAAC

101 I S V A V G L V S I R G V D S G L Y L G M N D K G E L

<-|-> Exon 3

TCTATGGATCAGAGAACTTACTCCGAATGCACTTTAGGAGCAGTTGAAGAGAACTGTATATAACACCTATTTCATCT

128 Y G S E K L T S E C I F R E Q F E E N W Y N T Y S S

AACATATATAACATGGAGACACTGGCGCAGGTATTTTGGCCACTTAACAAAGACGGAACCTCCACAGATGGCGCCAG

154 N I Y K H G D T G R R Y F V A L N K D G T P R D G A R

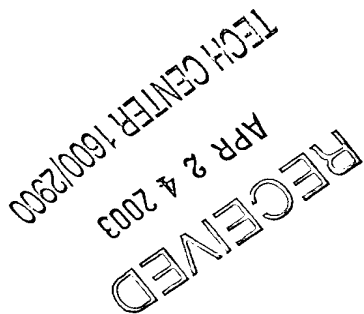
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181 S K R H Q K F T H F L P R P V D P E R V P E L Y K D L

TACTGATGTACACTTGA...

208 L M Y T

Fig. 13





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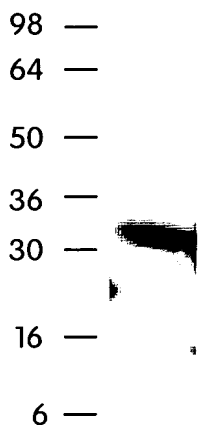


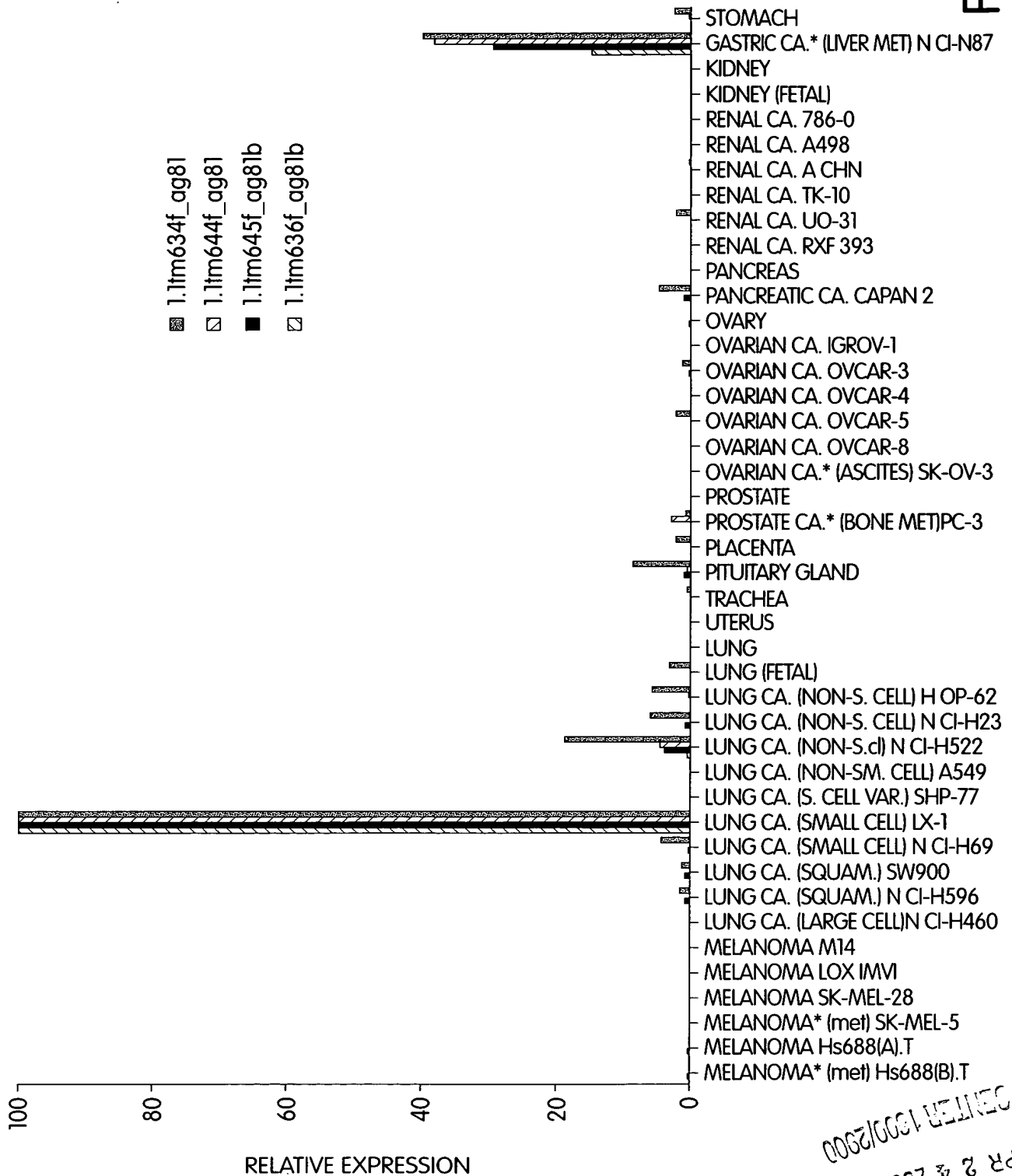
Fig. 14

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Fig. 15A



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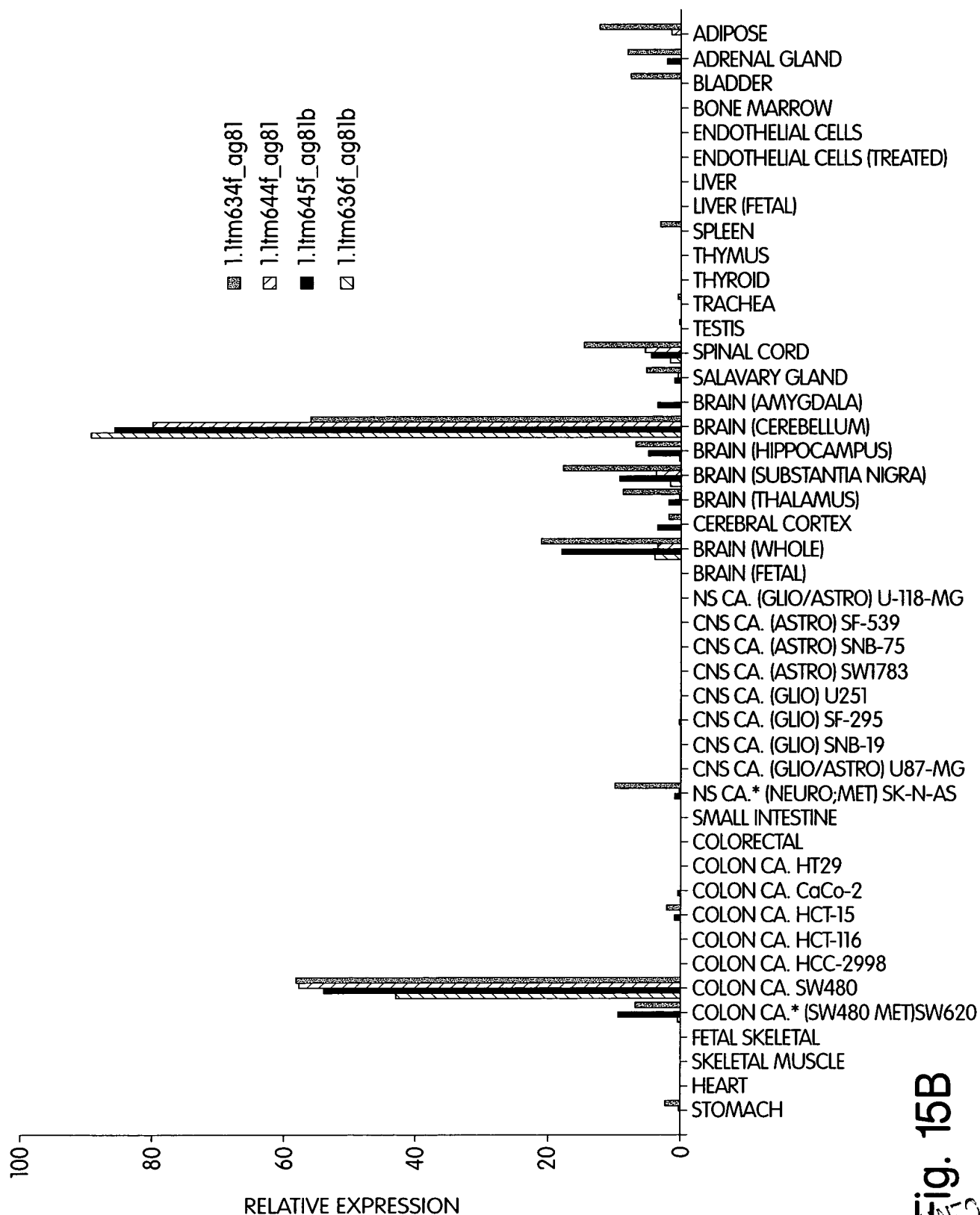


Fig. 15B

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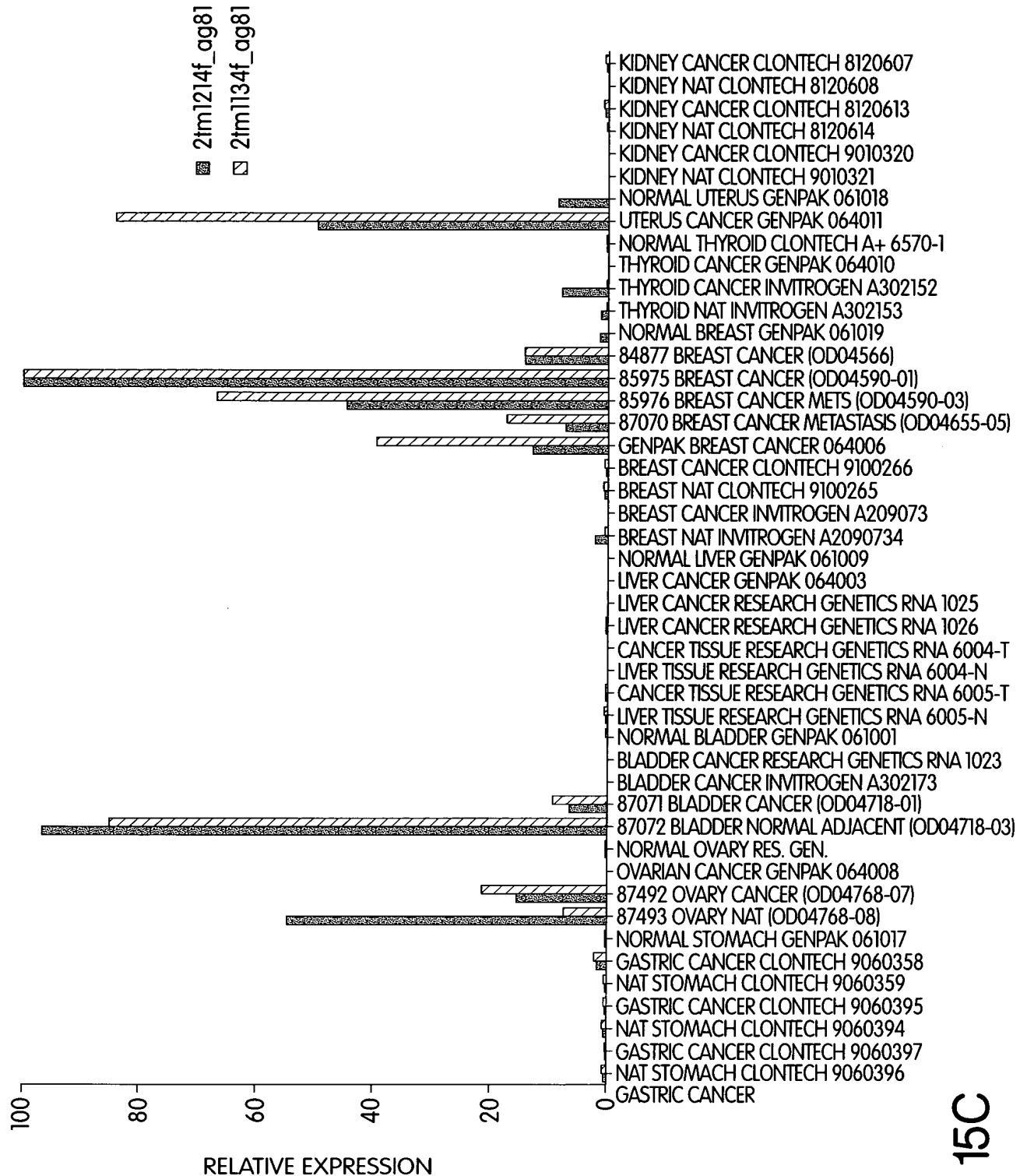
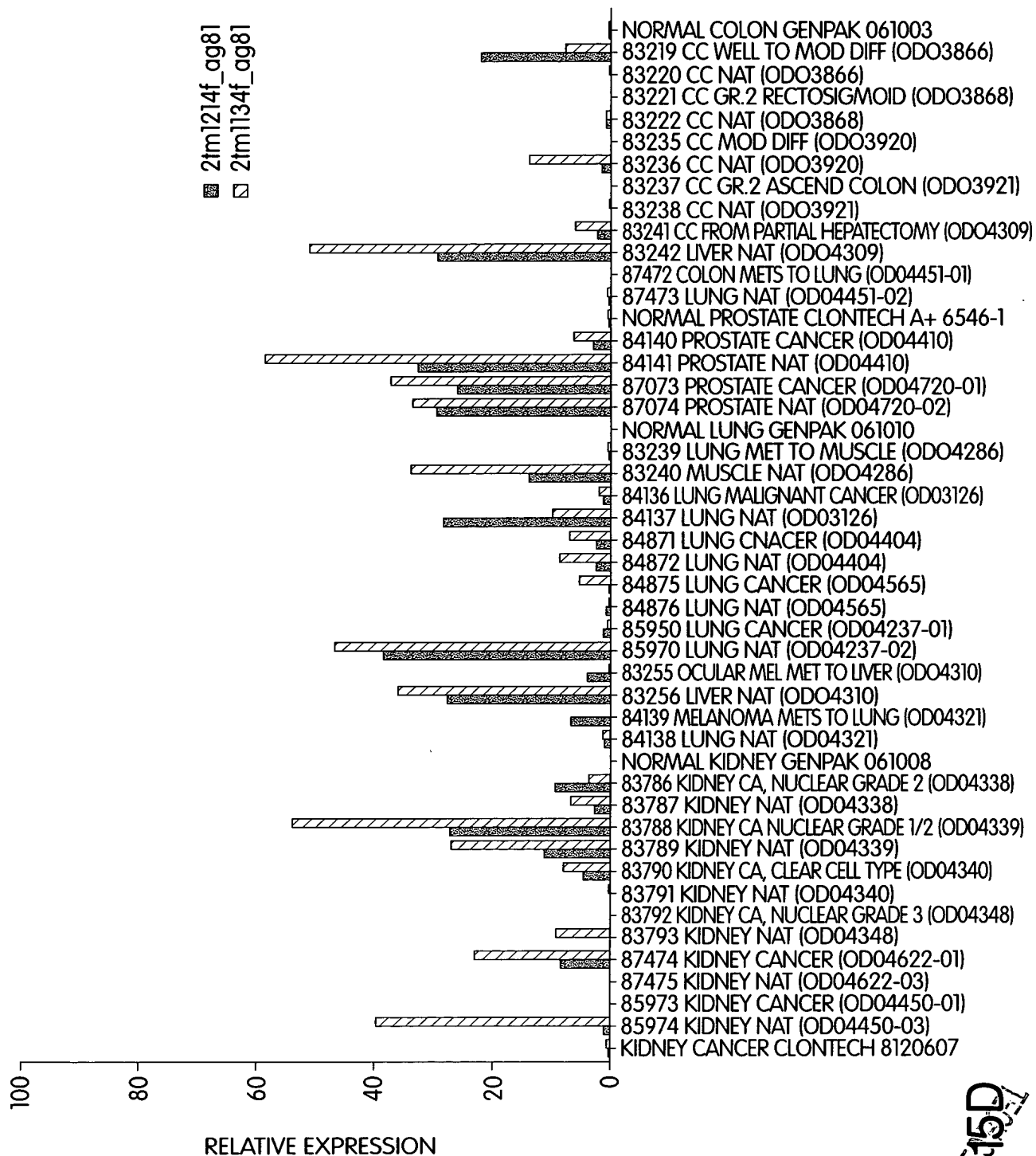


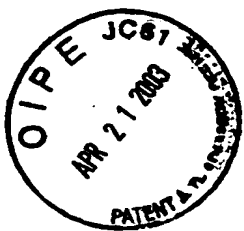
Fig. 15C



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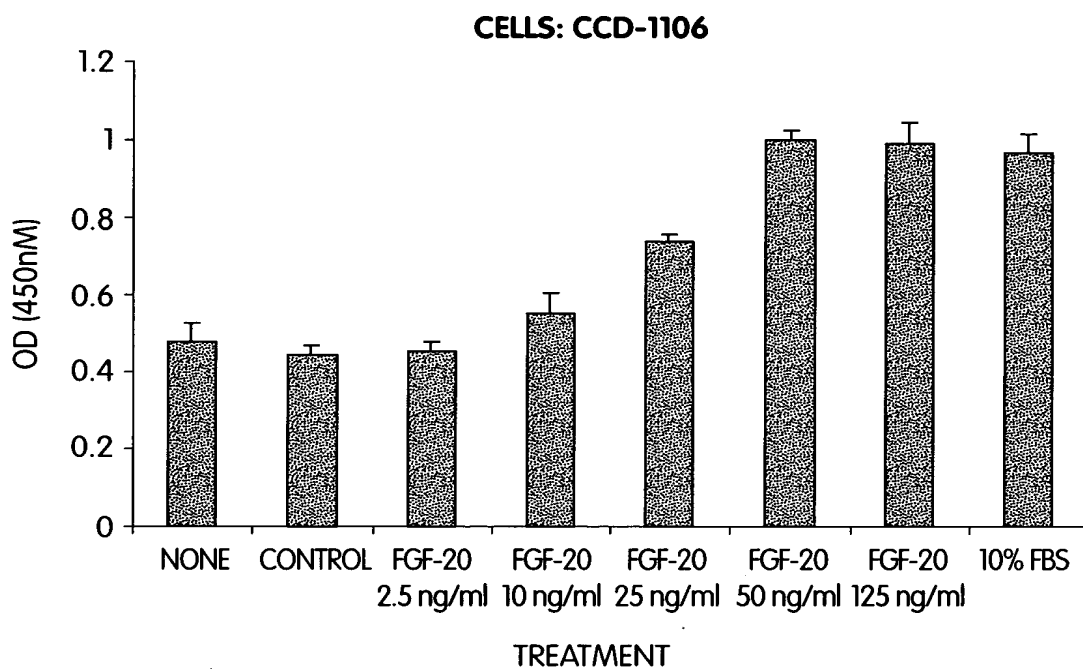


Fig. 16C

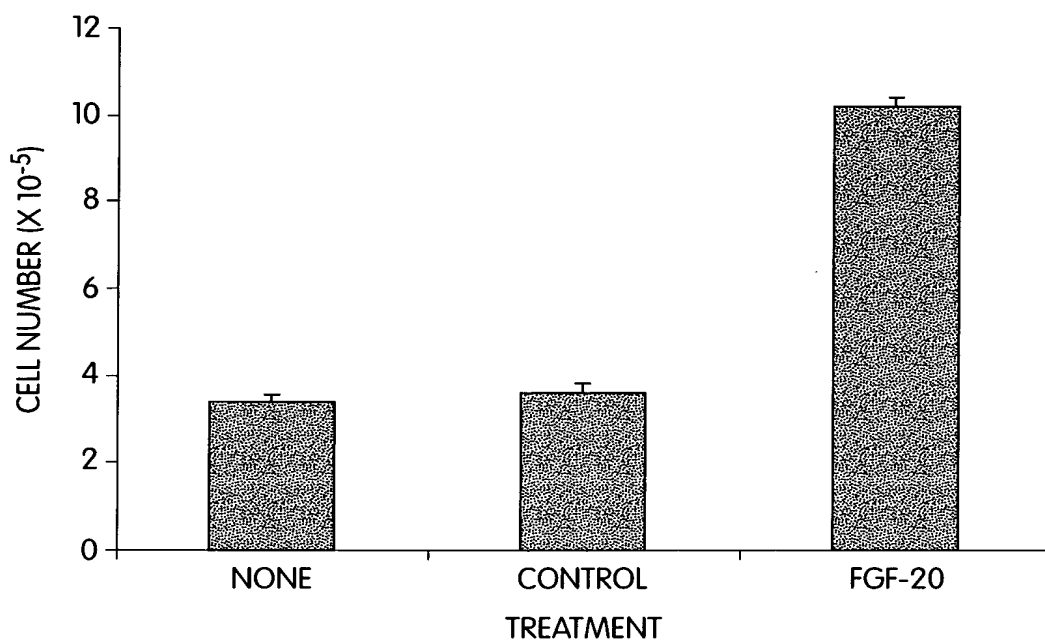


Fig. 17

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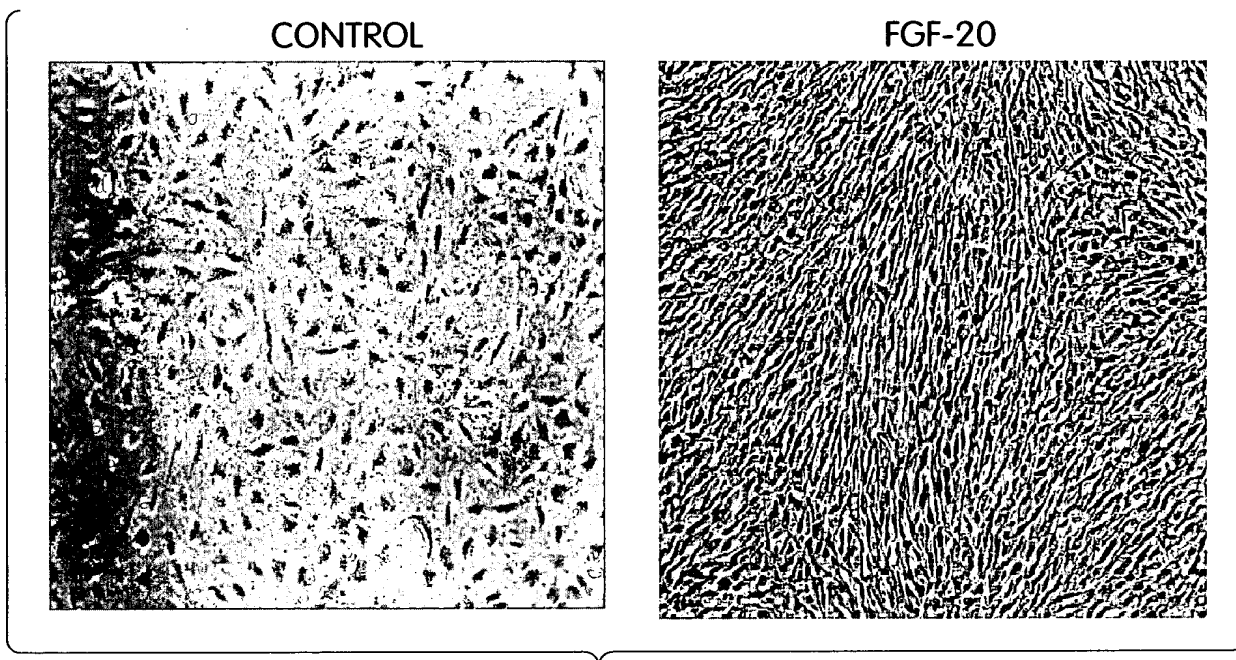
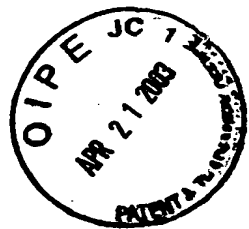


Fig. 18

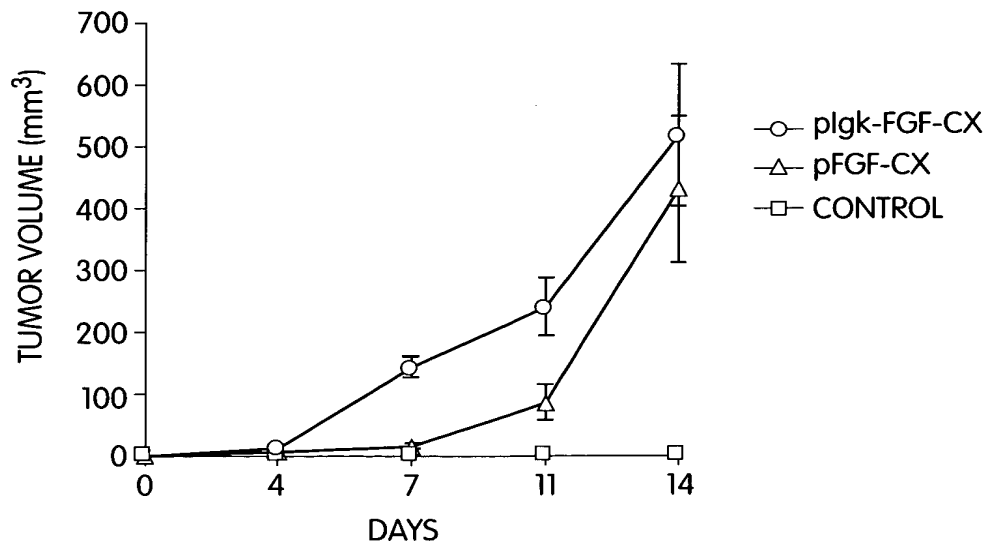
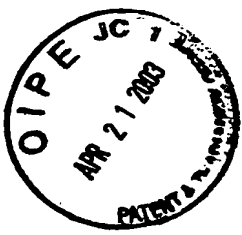


Fig. 19

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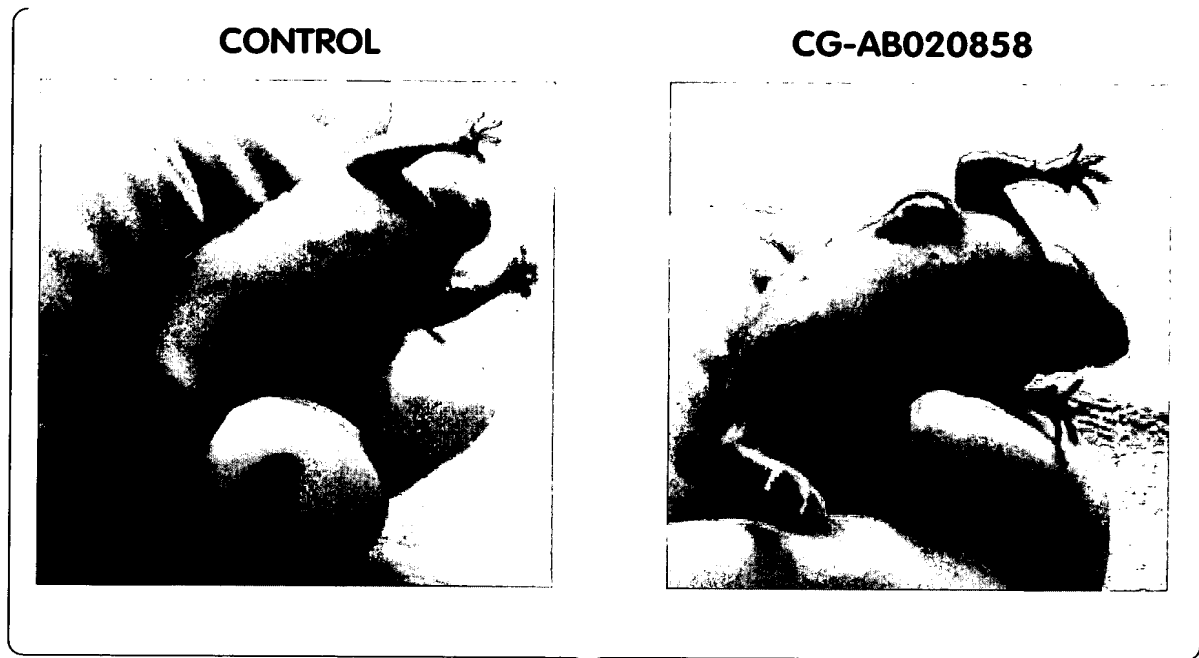


Fig. 20

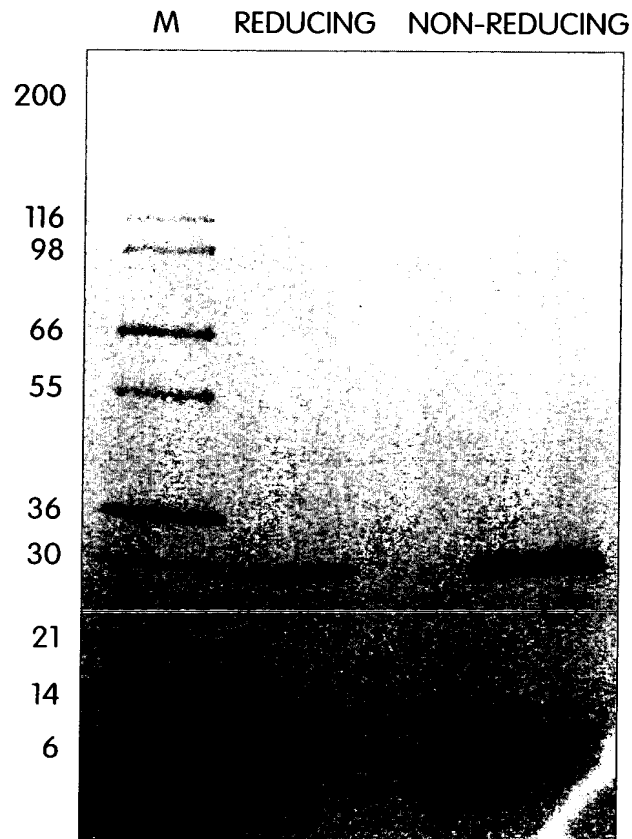


Fig. 21

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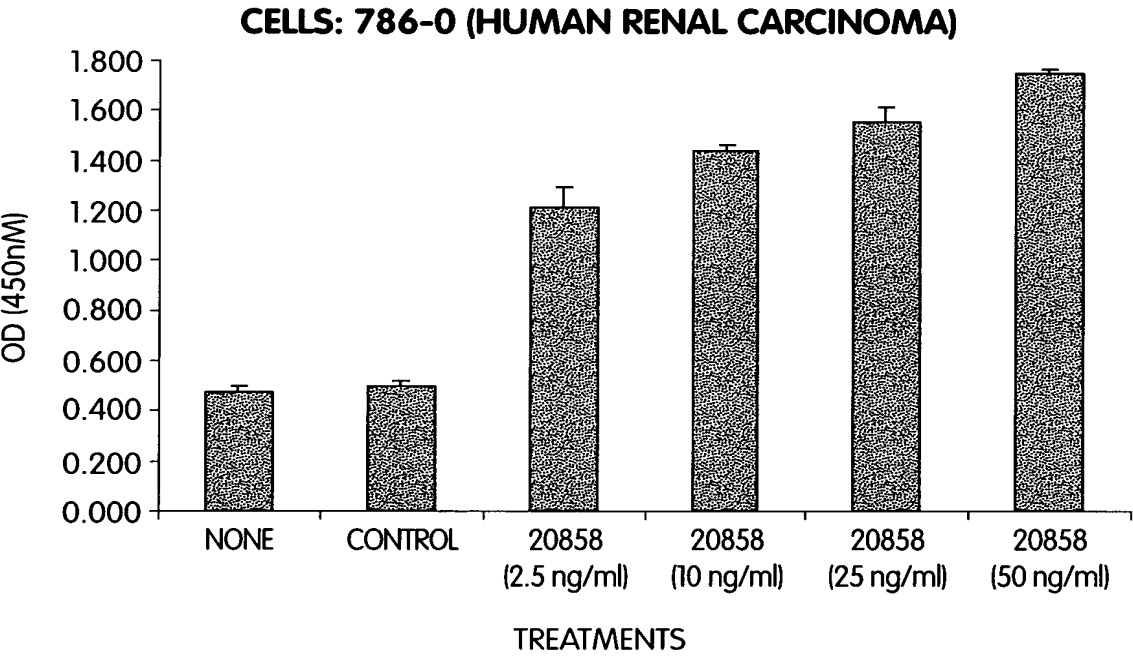


Fig. 22

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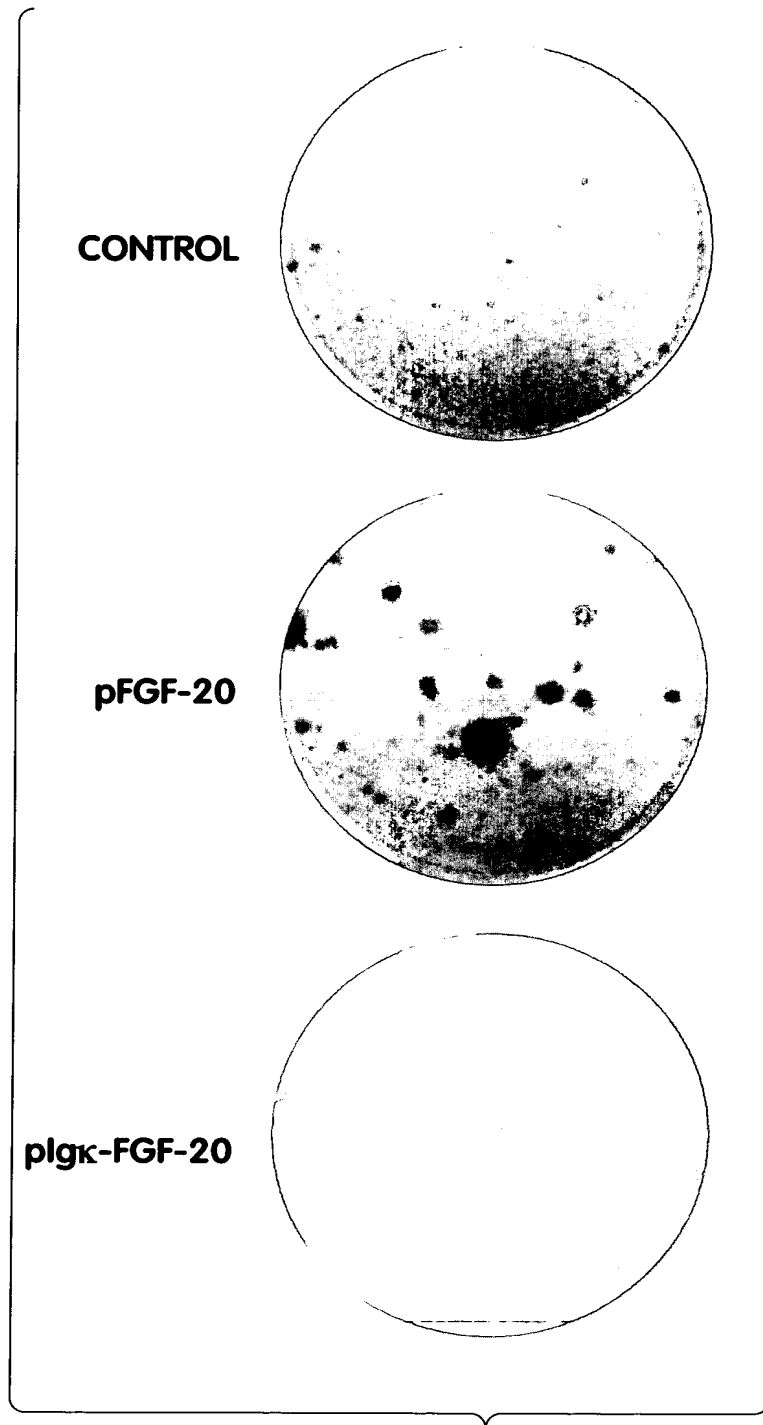


Fig. 23

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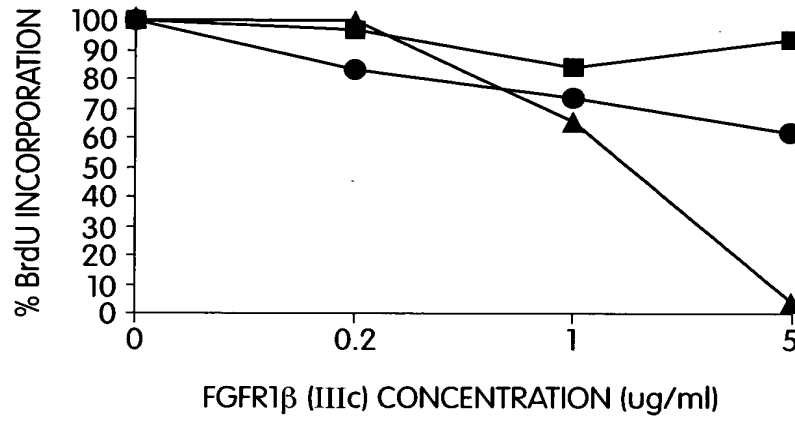


Fig. 24A

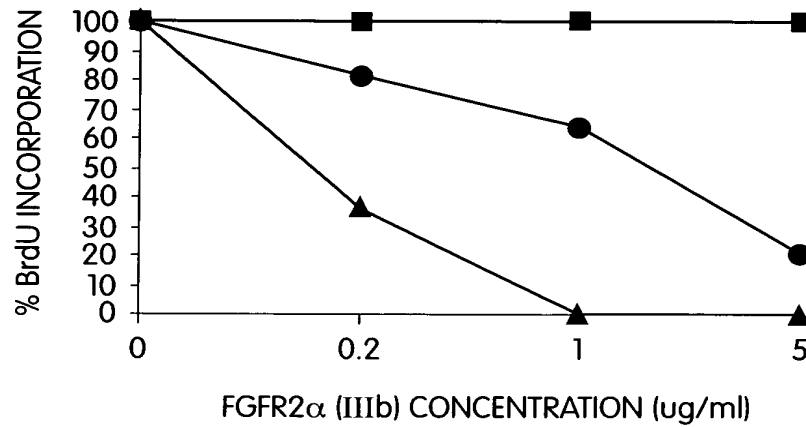
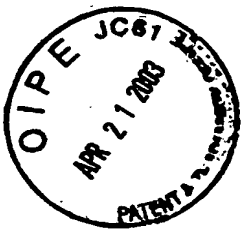


Fig. 24B

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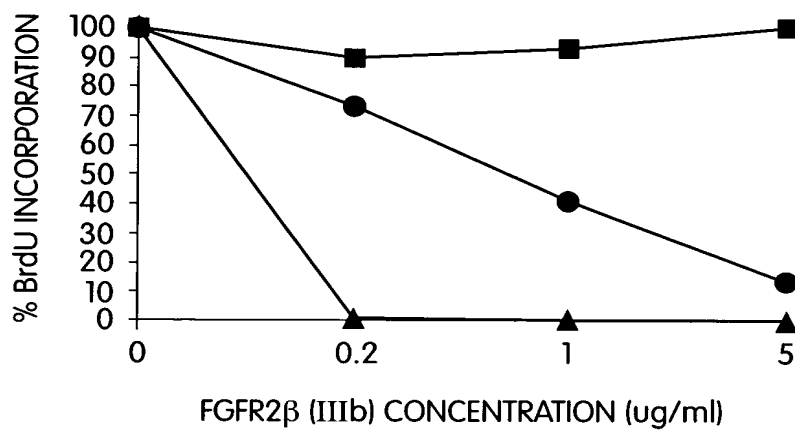


Fig. 24C

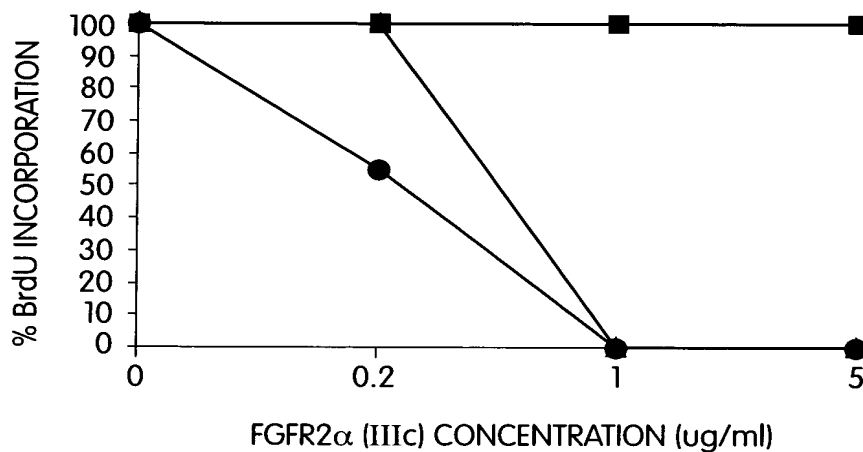


Fig. 24D

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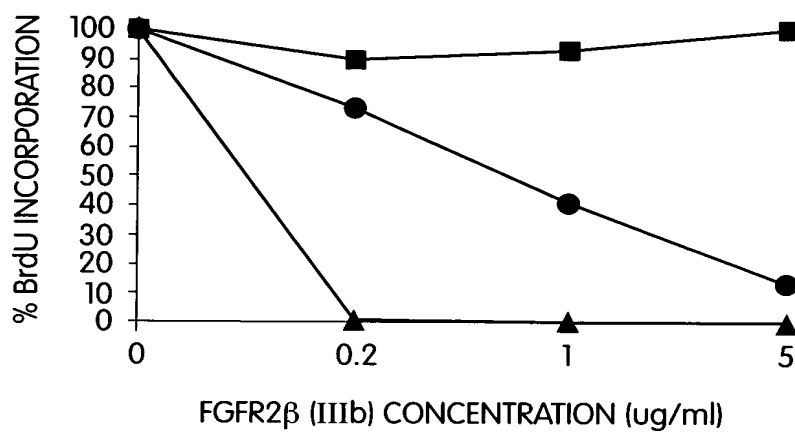


Fig. 24C

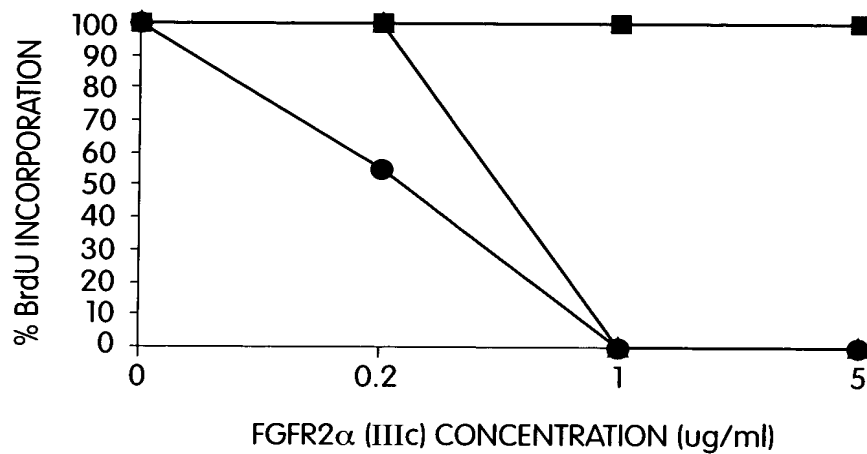


Fig. 24D

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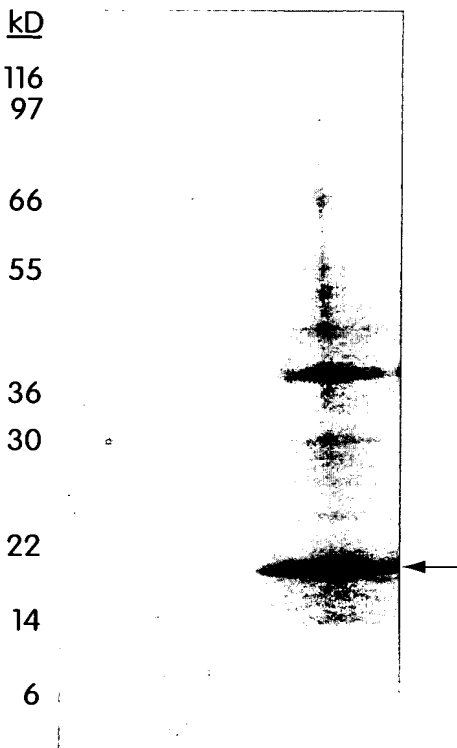


Fig. 25

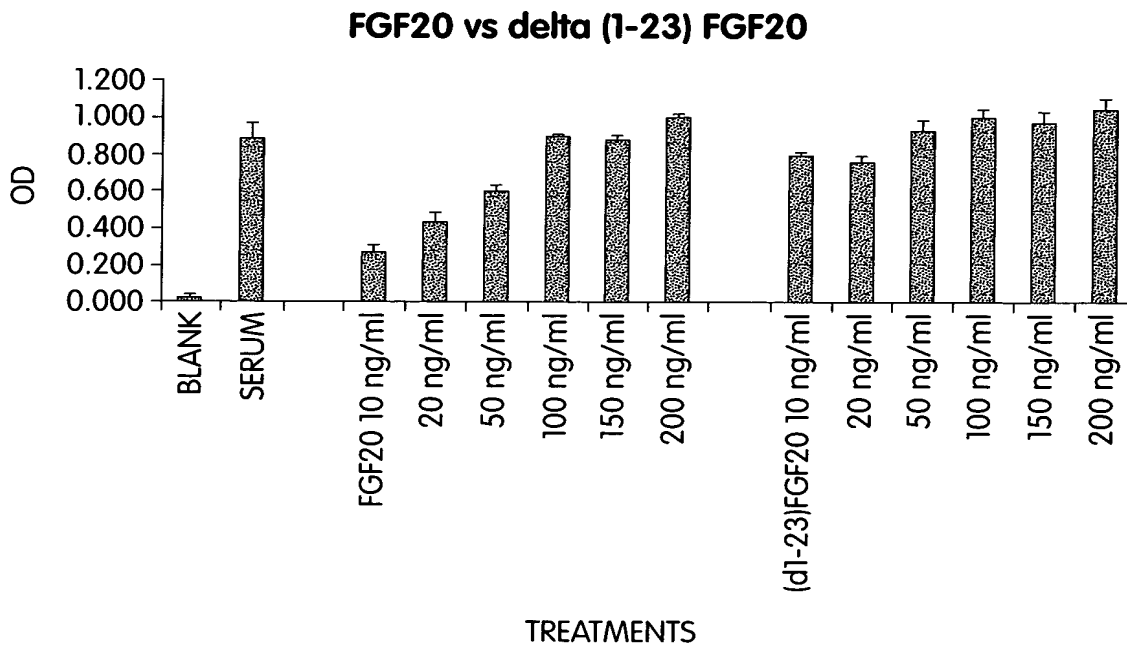


Fig. 26

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